

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/234,733DATE: 08/04/1999
TIME: 14:39:32

INPUT SET: S32774.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Jiang, Min
Potter, Andrew A.
MacLachlan, Philip R.

(ii) TITLE OF INVENTION: CAMP FACTOR OF STREPTOCOCCUS UBERIS

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Reed & Robins LLP
(B) STREET: 285 Hamilton Avenue, Suite 200
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94301

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/234,733
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/658,277
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Robins, Roberta L.
(B) REGISTRATION NUMBER: 33,208
(C) REFERENCE/DOCKET NUMBER: 9000-0030

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 327-3400
(B) TELEFAX: (415) 327 3231

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47
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 1191 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: single
52          (D) TOPOLOGY: linear
53
54      (ii) MOLECULE TYPE: DNA (genomic)
55
56
57      (ix) FEATURE:
58          (A) NAME/KEY: CDS
59          (B) LOCATION: 157..924
60
61
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64      AATGAACATA AAATAAAAAT TAATAATTAT ATATTTTATAT GATAATCACA TATATTTGAC      60
65
66      TTAAAAAAAT TGTACTGTA TGATACAGGC ATAAGTACTT ATTTATTTTA TAGATTGCAA      120
67
68      TTTATAAACA ATTATATTTT TCAAAGAGGA ATGCTT ATG GAA TTC AAA AAG TTA      174
69                                     Met Glu Phe Lys Lys Leu
70                                     1          5
71
72      CTT TAT TTA ACT GGT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT      222
73      Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile
74                                     10          15          20
75
76      TTA ACA AGT GTC CAA GCA AAT CAA ATA AAT GTT AGT CAA CCA TCT AAT      270
77      Leu Thr Ser Val Gln Ala Asn Gln Ile Asn Val Ser Gln Pro Ser Asn
78                                     25          30          35
79
80      AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA GAA GAA ATT GAT AAT AGT      318
81      Asn Glu Ser Asn Val Ile Ser Gln Lys Lys Glu Glu Ile Asp Asn Ser
82      40          45          50
83
84      CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT GTT AAA      366
85      Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp Val Lys
86      55          60          65          70
87
88      GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA      414
89      Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu
90      75          80          85
91
92      AAT TTA AAA ACT TCA CTT AGA GCT AAT CCT GAA ACA ATT TAT GAT TTA      462
93      Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu
94      90          95          100
95
96      AAT TCG ATT GGA ACA AGA GTA GAA GCA ATC TCT GAC GTG ATT CAA GCA      510
97      Asn Ser Glu Gln Thr Arg Val Glu Ala Ile Ser Asp Val Ile Gln Ala
    
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100  ATT GTT TTT TCA ACG CAA CAG TTA ACA AAT AAA GTT GAT CAA GCT CAC      558
101  Ile Val Phe Ser Thr Gln Gln Leu Thr Asn Lys Val Asp Gln Ala His
102      120                      125                      130
103
104  ATT GAT ATG GGA TTT GCT ATT ACG AAA TTA CTT ATT CGC ATT GCA GAC      606
105  Ile Asp Met Gly Phe Ala Ile Thr Lys Leu Leu Ile Arg Ile Ala Asp
106  135                      140                      145                      150
107
108  CCA TTT GCT TCA AAT GAA TCC ATT AAA GGG CAA GTC GAA GCT GTT AAA      654
109  Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys
110      155                      160                      165
111
112  CAA GTG CAA GCG ACT GTG CTT ACC TAT CCC GAT TTG CAG CCT ACG GAT      702
113  Gln Val Gln Ala Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp
114      170                      175                      180
115
116  AGA GCA ACT ATT TAC GTT AAA TCA AAA TTA GAC AAG CTT ATT TGG CAA      750
117  Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln
118      185                      190                      195
119
120  ACA AGA ATT ACC AGA GAT CAA AAA GTT CTT AAT GTA AAG AGT TTT GAA      798
121  Thr Arg Ile Thr Arg Asp Gln Lys Val Leu Asn Val Lys Ser Phe Glu
122      200                      205                      210
123
124  GTT TAT CAT CAA TTA AAT AAA GCT ATC ACA CAT GCA GTA GGT GTA CAA      846
125  Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly Val Gln
126  215                      220                      225                      230
127
128  TTA AAT CCA ACT GTA ACA GTT GCA CAA GTT GAC CAA GAA ATC AAA GTG      894
129  Leu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val
130      235                      240                      245
131
132  CTA CAA GAA GCA TTA AAT ACT GCT CTA CAG TAAGGTAGAG ATTGAATTGA      944
133  Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln
134      250                      255
135
136  CGTATTAAAA AGGACTGGAA TTTATTAATT TCAGTCCTTT AGAATTTTTA TTTAGCTGAT      1004
137
138  TTACTTGTTG AAGAGATTTG GTGGAAAATC AAGTACCATA CTTCAATTTCT CCTCCAAATA      1064
139
140  CTTGTATGTC GATTCCTTTC TAAACATAG CTAATTAGTT TAGTTTTCTG CCTAATAGAT      1124
141
142  TGTACATGAA ATTGTTCAAA ATTACTAGGG TAAAAGGTTT TTCTTTTAT AAATTCATCA      1184
143
144  TGACTAT      1191
145
146
147  (2) INFORMATION FOR SEQ ID NO:2:
148
149      (1) SEQUENCE CHARACTERISTICS:
150          (A) LENGTH: 256 amino acids

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153
154      (ii) MOLECULE TYPE: protein
155
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
157
158      Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile
159      1          5          10          15
160
161      Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn
162      20          25          30
163
164      Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys
165      35          40          45
166
167      Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala
168      50          55          60
169
170      Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser
171      65          70          75          80
172
173      Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro
174      85          90          95
175
176      Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile
177      100         105         110
178
179      Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn
180      115         120         125
181
182      Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu
183      130         135         140
184
185      Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
186      145         150         155         160
187
188      Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro
189      165         170         175
190
191      Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu
192      180         185         190
193
194      Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu
195      195         200         205
196
197      Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr
198      210         215         220
199
200      His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val
201      225         230         235         240
202
203      Ala Ile Phe Ala Thr Val Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln
  
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207 (2) INFORMATION FOR SEQ ID NO:3:

208

209 (i) SEQUENCE CHARACTERISTICS:

210 (A) LENGTH: 256 amino acids

211 (B) TYPE: amino acid

212 (C) STRANDEDNESS: single

213 (D) TOPOLOGY: linear

214

215 (ii) MOLECULE TYPE: protein

216

217

218

219

220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

221

222 Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile
223 1 5 10 15

224

225 Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn
226 20 25 30

227

228 Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys
229 35 40 45

230

231 Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala
232 50 55 60

233

234 Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser
235 65 70 75 80

236

237 Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro
238 85 90 95

239

240 Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile
241 100 105 110

242

243 Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn
244 115 120 125

245

246 Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu
247 130 135 140

248

249 Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
250 145 150 155 160

251

252 Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro
253 165 170 175

254

255 Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu
256 180 185 190

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
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PAGE: 1

SEQUENCE MISSING ITEM REPORT
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SEQUENCE CORRECTION REPORT
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Line	Original Text	Corrected Text
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